OIPE
OCT 04 2006
PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> Jung, Birgit
Mueller, Stefan
Kraut, Norbert

<120> Method for identifying compounds that inhibit or reduce a chronic inflammatory airway disease in which a macrophage is in a hyperactivated status due to down-regulated p21-activated kinase 2 (PAK2) kinase

<130> 1/1177

<140> 10/029,905
<141> 2001-12-21

<150> US 60/257,854
<151> 2000-12-22

<160> 12

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<211> 25
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 3
<211> 1819
<212> DNA
<213> Homo sapiens

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ccagaaattt ctcctccatc tgattttgag cacaccatcc atgttggctt tgatactgtt 180

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tccaacacag tgaagcagaa atatctgagc tttactcctc ctgagaaaga tggctttcct 360
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tatgaaaaaa ttggacaagg ggcttctggt acagttttca ctgctactga cgttgcactg 720
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<210> 4
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<212> PRT
<213> Homo sapiens

<400> 4

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Ala Asn His Ser Leu Lys Pro Leu Pro Ser Val Pro Glu Glu Lys Lys
         35                  40                  45

Pro Arg His Lys Ile Ile Ser Ile Phe Ser Gly Thr Glu Lys Gly Ser
     50                  55                  60

Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Pro Pro Ser Asp Phe
 65                  70                  75                  80

Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe Thr
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Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile Thr
            100                 105                 110
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Phe Tyr Asp Ser Asn Thr Val Lys Gln Lys Tyr Leu Ser Phe Thr Pro
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145 150 155 160

Gly Thr Glu Ala Pro Ala Val Val Thr Glu Glu Glu Asp Asp Asp Glu
165 170 175

Glu Thr Ala Pro Pro Val Ile Ala Pro Arg Pro Asp His Thr Lys Ser
180 185 190

Ile Tyr Thr Arg Ser Val Ile Asp Pro Val Pro Ala Pro Val Gly Asp
195 200 205

Ser His Val Asp Gly Ala Ala Lys Ser Leu Asp Lys Gln Lys Lys Lys
210 215 220

Pro Lys Met Thr Asp Glu Glu Ile Met Glu Lys Leu Arg Thr Ile Val
225 230 235 240

Ser Ile Gly Asp Pro Lys Lys Lys Tyr Thr Arg Tyr Glu Lys Ile Gly
245 250 255

Gln Gly Ala Ser Gly Thr Val Phe Thr Ala Thr Asp Val Ala Leu Gly
260 265 270

Gln Glu Val Ala Ile Lys Gln Ile Asn Leu Gln Lys Gln Pro Lys Lys
275 280 285

Glu Leu Ile Ile Asn Glu Ile Leu Val Met Lys Glu Leu Lys Asn Pro
290 295 300

Asn Ile Val Asn Phe Leu Asp Ser Tyr Leu Val Gly Asp Glu Leu Phe
305 310 315 320

Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu Thr Asp Val Val Thr
325 330 335

Glu Thr Cys Met Asp Glu Ala Gln Ile Ala Ala Val Cys Arg Glu Cys
340 345 350

Leu Gln Ala Leu Glu Phe Leu His Ala Asn Gln Val Ile His Arg Asp
355 360 365

Ile Lys Ser Asp Asn Val Leu Leu Gly Met Glu Gly Ser Val Lys Leu
370 375 380

Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro Glu Gln Ser Lys Arg
385 390 395 400

Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Val Thr
405 410 415

Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp Ser Leu Gly Ile Met
420 425 430

Ala Ile Glu Met Val Glu Gly Glu Pro Pro Tyr Leu Asn Glu Asn Pro
435 440 445

Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly Thr Pro Glu Leu Gln
450 455 460

Asn Pro Glu Lys Leu Ser Pro Ile Phe Arg Asp Phe Leu Asn Arg Cys
465 470 475 480

Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala Lys Glu Leu Leu Gln
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His Pro Phe Leu Lys Leu Ala Lys Pro Leu Ser Ser Leu Thr Pro Leu
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Ile Met Ala Ala Lys Glu Ala Met Lys Ser Asn Arg
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 7
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
aagaattctc atgtctgata acggagaact g 31

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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tttctagaac ggttactctt cattgcttc 29

<210> 9
<211> 3255
<212> DNA
<213> Homo sapiens

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gatacaatgg tgcagcagaa attggatgat atcaaggatc gaattaagag agaaataagg 180
aaagaactga aaatcaaaga aggagctgaa aatctgagga aagtcacaac agataaaaaa 240
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<211> 984
<212> PRT
<213> Homo sapiens

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35 40 45

Lys Asp Arg Ile Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu
50 55 60

Gly Ala Glu Asn Leu Arg Lys Val Thr Thr Asp Lys Lys Ser Leu Ala
65 70 75 80

Tyr Val Asp Asn Ile Leu Lys Lys Ser Asn Lys Lys Leu Glu Glu Leu
85 90 95

His His Lys Leu Gln Glu Leu Asn Ala His Ile Val Val Ser Asp Pro
100 105 110

Glu Asp Ile Thr Asp Cys Pro Arg Thr Pro Asp Thr Pro Asn Asn Asp
115 120 125

Pro Arg Cys Ser Thr Ser Asn Asn Arg Leu Lys Ala Leu Gln Lys Gln
130 135 140

Leu Asp Ile Glu Leu Lys Val Lys Gln Gly Ala Glu Asn Met Ile Gln
145 150 155 160

Met Tyr Ser Asn Gly Ser Ser Lys Asp Arg Lys Leu His Gly Thr Ala
165 170 175

Gln Gln Leu Leu Gln Asp Ser Lys Thr Lys Ile Glu Val Ile Arg Met
180 185 190

Gln Ile Leu Gln Ala Val Gln Thr Asn Glu Leu Ala Phe Asp Asn Ala
195 200 205

Lys Pro Val Ile Ser Pro Leu Glu Leu Arg Met Glu Glu Leu Arg His
210 215 220

His Phe Arg Ile Glu Phe Ala Val Ala Glu Gly Ala Lys Asn Val Met
225 230 235 240

Lys Leu Leu Gly Ser Gly Lys Val Thr Asp Arg Lys Ala Leu Ser Glu
245 250 255

Ala Gln Ala Arg Phe Asn Glu Ser Ser Gln Lys Leu Asp Leu Leu Lys
260 265 270

Tyr Ser Leu Glu Gln Arg Leu Asn Glu Val Pro Lys Asn His Pro Lys
275 280 285

Ser Arg Ile Ile Ile Glu Glu Leu Ser Leu Val Ala Ala Ser Pro Thr
290 295 300

Leu Ser Pro Arg Gln Ser Met Ile Ser Thr Gln Asn Gln Tyr Ser Thr
305 310 315 320

Leu Ser Lys Pro Ala Ala Leu Thr Gly Thr Leu Glu Val Arg Leu Met
325 330 335

Gly Cys Gln Asp Ile Leu Glu Asn Val Pro Gly Arg Ser Lys Ala Thr
340 345 350

Ser Val Ala Leu Pro Gly Trp Ser Pro Ser Glu Thr Arg Ser Ser Phe
355 360 365

Met Ser Arg Thr Ser Lys Ser Lys Ser Gly Ser Ser Arg Asn Leu Leu
370 375 380

Lys Thr Asp Asp Leu Ser Asn Asp Val Cys Ala Val Leu Lys Leu Asp
385 390 395 400

Asn Thr Val Val Gly Gln Thr Ser Trp Lys Pro Ile Ser Asn Gln Ser
405 410 415

Trp Asp Gln Lys Phe Thr Leu Glu Leu Asp Arg Ser Arg Glu Leu Glu
420 425 430

Ile Ser Val Tyr Trp Arg Asp Trp Arg Ser Leu Cys Ala Val Lys Phe
435 440 445

Leu Arg Leu Glu Asp Phe Leu Asp Asn Gln Arg His Gly Met Cys Leu
450 455 460

Tyr Leu Glu Pro Gln Gly Thr Leu Phe Ala Glu Val Thr Phe Phe Asn
465 470 475 480

Pro Val Ile Glu Arg Arg Pro Lys Leu Gln Arg Gln Lys Lys Ile Phe
485 490 495

Ser Lys Gln Gln Gly Lys Thr Phe Leu Arg Ala Pro Gln Met Asn Ile
500 505 510

Asn Ile Ala Thr Trp Gly Arg Leu Val Arg Arg Ala Ile Pro Thr Val
515 520 525

Asn His Ser Gly Thr Phe Ser Pro Gln Ala Pro Val Pro Thr Thr Val
530 535 540

Pro Val Val Asp Val Arg Ile Pro Gln Leu Ala Pro Pro Ala Ser Asp
545 550 555 560

Ser Thr Val Thr Lys Leu Asp Phe Asp Leu Glu Pro Glu Pro Pro Pro
565 570 575

Ala Pro Pro Arg Ala Ser Ser Leu Gly Glu Ile Asp Glu Ser Ser Glu
580 585 590

Leu Arg Val Leu Asp Ile Pro Gly Gln Asp Ser Glu Thr Val Phe Asp
595 600 605

Ile Gln Asn Asp Arg Asn Ser Ile Leu Pro Lys Ser Gln Ser Glu Tyr
610 615 620

Lys Pro Asp Thr Pro Gln Ser Gly Leu Glu Tyr Ser Gly Ile Gln Glu
625 630 635 640

Leu Glu Asp Arg Arg Ser Gln Gln Arg Phe Gln Phe Asn Leu Gln Asp
645 650 655

Phe Arg Cys Cys Ala Val Leu Gly Arg Gly His Phe Gly Lys Val Leu
660 665 670

Leu Ala Glu Tyr Lys Asn Thr Asn Glu Met Phe Ala Ile Lys Ala Leu
675 680 685

Lys Lys Gly Asp Ile Val Ala Arg Asp Glu Val Asp Ser Leu Met Cys
690 695 700

Glu Lys Arg Ile Phe Glu Thr Val Asn Ser Val Arg His Pro Phe Leu
705 710 715 720

Val Asn Leu Phe Ala Cys Phe Gln Thr Lys Glu His Val Cys Phe Val
725 730 735

Met Glu Tyr Ala Ala Gly Gly Asp Leu Met Met His Ile His Thr Asp
740 745 750

Val Phe Ser Glu Pro Arg Ala Val Phe Tyr Ala Ala Cys Val Val Leu
755 760 765

Gly Leu Gln Tyr Leu His Glu His Lys Ile Val Tyr Arg Asp Leu Lys
770 775 780

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Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly Phe Val Lys Ile Ala Asp
785                 790                 795                 800

Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr Gly Asp Arg Thr Ser Thr
                805                 810                 815

Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro Glu Val Leu Thr Glu Thr
            820                 825                 830

Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly Leu Gly Val Leu Ile Tyr
        835                 840                 845

Glu Met Leu Val Gly Glu Ser Pro Phe Pro Gly Asp Asp Glu Glu Glu
    850                 855                 860

Val Phe Asp Ser Ile Val Asn Asp Glu Val Arg Tyr Pro Arg Phe Leu
865                 870                 875                 880

Ser Thr Glu Ala Ile Ser Ile Met Arg Arg Leu Leu Arg Arg Asn Pro
                885                 890                 895

Glu Arg Arg Leu Gly Ala Ser Glu Lys Asp Ala Glu Asp Val Lys Lys
            900                 905                 910

His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala Leu Met Asp Lys Lys
        915                 920                 925

Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly Arg Glu Asp Val Ser
    930                 935                 940

Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro Ile Leu Thr Pro Pro
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Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Phe Arg Asp
                965                 970                 975

Phe Asp Tyr Ile Ala Asp Trp Cys
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<213> Homo sapiens

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<211> 197
<212> PRT
<213> Homo sapiens

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Gly Phe Ser Val Ser His Thr Thr Arg Asn Pro Arg Pro Gly Glu Glu
35 40 45

Asn Gly Lys Asp Tyr Tyr Phe Val Thr Arg Glu Val Met Gln Arg Asp
50 55 60

Ile Ala Ala Gly Asp Phe Ile Glu His Ala Glu Phe Ser Gly Asn Leu
65 70 75 80

Tyr Gly Thr Ser Lys Val Ala Val Gln Ala Val Gln Ala Met Asn Arg
85 90 95

Ile Cys Val Leu Asp Val Asp Leu Gln Gly Val Arg Asn Ile Lys Ala
100 105 110

Thr Asp Leu Arg Pro Ile Tyr Ile Ser Val Gln Pro Pro Ser Leu His
115 120 125

Val Leu Glu Gln Arg Leu Arg Gln Arg Asn Thr Glu Thr Glu Glu Ser
130 135 140

Leu Val Lys Arg Leu Ala Ala Ala Gln Ala Asp Met Glu Ser Ser Lys
145 150 155 160

Glu Pro Gly Leu Phe Asp Val Val Ile Ile Asn Asp Ser Leu Asp Gln
165 170 175

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Gln Arg Thr Gly Ala
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<212> PRT
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<220>
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